



1600

RAW SEQUENCE LISTING

DATE: 06/12/2003

PATENT APPLICATION: US/09/765,061D

TIME: 09:02:28

Input Set : A:\UTHou-16UTL 79-88.ST25.txt Output Set: N:\CRF4\06122003\I765061D.raw

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3 <110> APPLICANT: The Board of Regents of the University of Texas System
      5 <120>. TITLE OF INVENTION: MUTATIONS IN A NOVEL PHOTORECEPTOR-PINEAL GENE ON 17P CAUSE
LEBER
               CONGENITAL AMAUROSIS (LCA4)
      8 <130> FILE REFERENCE: 96606/16UTL
                                                                         Doos Not Comply
     10 <140> CURRENT APPLICATION NUMBER: 09/765,061D
                                                                     Corrected Diskette Needed
     11 <141> CURRENT FILING DATE: 2001-01-17
     13 <150> PRIOR APPLICATION NUMBER: 60/331362
                                                                 Seq. Nos. 79-88) invalid,

Per 1. 825 of

Sequence Rules.

"Any anerdment to the

paper copy of the Sequence Listing

must be accommend.
     14 <151> PRIOR FILING DATE: 2001-01-04
     16 <160> NUMBER OF SEQ ID NOS: 10 additional sequences, Seq. Nos. 79-88
     18 <170> SOFTWARE: PatentIn version 3.2
                                         por previously
submitted CRF.
     20 <210> SEQ ID NO: 79
     21 <211> LENGTH: 34
     22 <212> TYPE: DNA
     23 <213> ORGANISM: Homo sapiens
     26 <220> FEATURE:
     27 <221> NAME/KEY: misc_feature
                                                                   must be accompanied by a
     28 <222> LOCATION: (1)..(34)
     29 <223> OTHER INFORMATION: Donor Splice Site: Residue 1-10 are the exonic sequence and
               Residues 11-34 are the intronic sequence
     32 <400> SEQUENCE: 79
     33 cggatcccga gtgagtgggg ccctccggag caga
     36 <210> SEQ ID NO: 80
    37 <211> LENGTH: 35
     38 <212> TYPE: DNA
     39 <213> ORGANISM: Homo sapiens
     42 <220> FEATURE:
     43 <221> NAME/KEY: misc_feature
     44 <222> LOCATION: (1)..(35)
     45 <223> OTHER INFORMATION: Acceptor Splice Site: Residues 1-25 are the intronic sequence
               and Residues 26-35 are the exonic sequence.
     48 <400> SEQUENCE: 80
     49 cagagtgcac cgtctcggtg actaggtgat ctttc
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     52 <210> SEQ ID NO: 81
     53 <211> LENGTH: 35
     54 <212> TYPE: DNA
     55 <213> ORGANISM: Homo sapiens
     58 <220> FEATURE:
     59 <221> NAME/KEY: misc feature
     60 <222> LOCATION: (1)..(35)
     61 <223> OTHER INFORMATION: Donor Splice Site: Residue 1-10 are the exonic sequence and
              Residues 11-35 are the intronic sequence
     64 <400> SEQUENCE: 81
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65 csacaccatc gtaagtaggc cctgcgcgcc tgtct

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/765,0610

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Input Set : A:\UTHou-16UTL 79-88.ST25.txt
Output Set: N:\CRF4\06122003\I765061D..raw

68 <210> SEQ ID NO: 82 69 <211> LENGTH: 35 70 <212> TYPE: DNA 71 <213> ORGANISM: Homo sapiens 74 <220> FEATURE: . 75 <221> NAME/KEY: misc feature 76 <222> LOCATION: (1)..(35) 77 <223> OTHER INFORMATION: Acceptor Splice Site: Residues 1-25 are the intronic sequence 78 and Residues 26-35 are the exonic sequence. 80 <400> SEQUENCE: 82 81 gccatccatc cgtttatccc cacagcacac ggggg 35 84 <210> SEQ ID NO: 83 85 <211> LENGTH: 35 86 <212> TYPE: DNA 87 <213> ORGANISM: Homo sapiens 90 <220> FEATURE: 91 <221> NAME/KEY: misc feature 92 <222> LOCATION: (1)..(35) 93 <223> OTHER INFORMATION: Donor Splice Site: Residue 1-10 are the exonic sequence and Residues 11-35 are the intronic sequence 96 <400> SEQUENCE: 83 97 gctgctgcag gtggggctgg ggttggcagg gctgg 35 100 <210> SEQ ID NO: 84 101 <211> LENGTH: 35 102 <212> TYPE: DNA 103 <213> ORGANISM: Homo sapiens 106 <220> FEATURE: 107 <221> NAME/KEY: misc feature 108 <222> LOCATION: (1)..(35) 109 <223> OTHER INFORMATION: Acceptor Splice Site: Residues 1-25 are the intronic sequence 110 and Residues 26-35 are the exonic sequence. 112 <400> SEQUENCE: 84 113 cactgacctg cagctctggg gccaggttga tgccc 35 116 <210> SEQ ID NO: 85 117 <211> LENGTH: 35 118 <212> TYPE: DNA 119 <213> ORGANISM: Homo sapiens 122 <220> FEATURE: 123 <221> NAME/KEY: misc feature 124 <222> LOCATION: (1)..(35) 125 <223> OTHER INFORMATION: Donor Splice Site: Residue 1-10 are the exonic sequence and 126 Residues 11-35 are the intronic sequence 128 <400> SEQUENCE: 85 129 gcagaccaag gtcagaggcc gctggccacg gggtg 35 132 <210> SEQ ID NO: 86 133 <211> LENGTH: 35

134 <212> TYPE: DNA

138 <220> FEATURE:

135 <213> ORGANISM: Homo sapiens





RAW SEQUENCE LISTING

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- 139 <221> NAME/KEY: misc_feature
- 140 <222> LOCATION: (1)..(35)
- 141 <223> OTHER INFORMATION: Acceptor Splice Site: Residues 1-25 are the intronic sequence
 - and Residues 26-35 are the exonic sequence.
 - 144 <400> SEQUENCE: 86
 - 145 catggctgac cttctccctg ggcaggagaa gccrt
 - 148 <210> SEQ ID NO: 87
 - 149 <211> LENGTH: 35
 - 150 <212> TYPE: DNA
 - 151 <213> ORGANISM: Homo sapiens
 - 154 <220> FEATURE:
 - 155 <221> NAME/KEY: misc feature
 - 156 <222> LOCATION: (1)..(35)
 - 157 <223> OTHER INFORMATION: Donor Splice Site: Residue 1-10 are the exonic sequence and
 - Residues 11-35 are the intronic sequence
 - 160 <400> SEQUENCE: 87
 - 161 caccaccag gtgcgcgggg ctgcaggggc ggaca
 - 164 <210> SEQ ID NO: 88
 - 165 <211> LENGTH: 35
 - 166 <212> TYPE: DNA
 - 167 <213> ORGANISM: Homo sapiens
 - 170 <220> FEATURE:
 - 171 <221> NAME/KEY: misc_feature
 - 172 <222> LOCATION: (1)..(35)
- 173 < 223 > OTHER INFORMATION: Acceptor Splice Site: Residues 1-25 are the intronic sequence
 - and Residues 26-35 are the exonic sequence.
 - 176 <400> SEQUENCE: 88
 - 177 getggatget eeetgeteee cacaggeate gtgaa

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/765,0610

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Input Set : A:\UTHou-16UTL 79-88.ST25.txt
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